

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: INCYTE PHARMACEUTICALS, INC.
- (ii) TITLE OF THE INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) pct APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: us 08/773,870
  - (B) FILING DATE: 27-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0179 PCT
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 411 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: Consensus

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(B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Phe	Pro	Arg	Pro	Lys	Lys	Asn	Leu	Pro	Gln	Pro	Lys	Xaa	Ala
1				5				10						15	
Ala	Thr	Glu	Gly	Pro	Ser	Ala	Ala	Ser	Gly	Val	Pro	Gln	Thr	Gly	Pro
			20					25					30		
Gly	Arg	Glu	Val	Ala	Ala	Thr	Arg	Pro	Lys	Thr	Thr	Lys	Ser	Gly	Lys
		35					40					45			
Ala	Leu	Ala	Lys	Thr	Arg	Trp	Val	Glu	Pro	Gln	Asn	Val	Val	Ala	Ala
	50					55				60					
Ala	Ala	Ala	Lys	Ala	Lys	Met	Ala	Thr	Ser	Ile	Pro	Glu	Pro	Glu	Gly
65					70				75					80	
Ala	Ala	Ala	Ala	Thr	Ala	Gln	His	Ser	Ala	Glu	Pro	Trp	Ala	Arg	Met
			85					90					95		
Gly	Gly	Lys	Arg	Thr	Lys	Lys	Ser	Lys	His	Leu	Asp	Asp	Glu	Tyr	Glu
		100						105					110		
Ser	Ser	Glu	Glu	Arg	Glu	Thr	Pro	Ala	Val	Pro	Pro	Thr	Trp	Arg	
	115					120						125			
Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Arg	Ala	Gln	Leu	Ala	Pro	Arg	Pro
	130					135					140				
Pro	Met	Ala	Pro	Arg	Ser	Gln	Ile	Pro	Ser	Arg	His	Val	Leu	Cys	Leu
145					150					155				160	
Pro	Pro	Arg	Asn	Val	Thr	Leu	Leu	Gln	Glu	Arg	Ala	Asn	Lys	Leu	Val
			165					170					175		
Lys	Tyr	Leu	Met	Ile	Lys	Asp	Tyr	Lys	Lys	Ile	Pro	Ile	Lys	Arg	Ala
		180						185					190		
Asp	Met	Leu	Lys	Asp	Val	Ile	Arg	Glu	Tyr	Asp	Glu	His	Phe	Pro	Glu
	195						200					205			
Ile	Ile	Glu	Arg	Ala	Thr	Tyr	Thr	Leu	Glu	Lys	Lys	Phe	Gly	Ile	His
	210					215					220				
Leu	Lys	Glu	Ile	Asp	Lys	Glu	Glu	His	Leu	Tyr	Ile	Leu	Val	Cys	Thr
225					230					235				240	
Arg	Asp	Ser	Ser	Ala	Arg	Leu	Leu	Gly	Lys	Thr	Lys	Asp	Thr	Pro	Arg
			245					250					255		
Leu	Ser	Leu	Leu	Leu	Val	Ile	Leu	Gly	Val	Ile	Phe	Met	Asn	Gly	Asn
		260						265					270		
Arg	Ala	Ser	Glu	Ala	Val	Leu	Trp	Glu	Ala	Leu	Arg	Lys	Met	Gly	Leu
	275						280					285			
Arg	Pro	Gly	Val	Arg	His	Pro	Leu	Leu	Gly	Asp	Leu	Arg	Lys	Leu	Leu
	290					295					300				
Thr	Tyr	Glu	Phe	Val	Lys	Gln	Lys	Tyr	Leu	Asp	Tyr	Arg	Arg	Val	Pro
305					310					315				320	
Asn	Ser	Asn	Pro	Pro	Glu	Tyr	Glu	Phe	Leu	Trp	Gly	Leu	Arg	Ser	Tyr
			325					330					335		
His	Glu	Thr	Ser	Lys	Met	Lys	Val	Leu	Arg	Phe	Ile	Ala	Glu	Val	Gln
		340						345					350		
Lys	Arg	Asp	Pro	Arg	Asp	Trp	Thr	Ala	Gln	Phe	Met	Glu	Ala	Ala	Asp
	355					360					365				
Glu	Ala	Leu	Asp	Ala	Leu	Asp	Ala	Ala	Ala	Ala	Glu	Ala	Glu	Ala	Arg
	370					375					380				
Ala	Glu	Ala	Arg	Thr	Arg	Met	Gly	Ile	Gly	Asp	Glu	Ala	Val	Ser	Gly
385					390					395				400	
Pro	Gly	Ala	Gly	Met	Thr	Leu	Ser	Leu	Ser	Cys					

405

410

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CNACGNGAAT	GGCCTTCCCCG	CGCCCCAAGA	AGAACCTGCC	CCAGCCCAAG	NAGGCTGCCA	60
CAGAGGGCCC	CAGTGTGCC	TCTGGTGTGC	CCCAGACGGG	ACCTGGCAGG	GAGGTGGCAG	120
CCACCCGGCC	CAAGACCACC	AAGTCGGGGA	AGGCGCTGGC	CAAGACTCGG	TGGGTGGAGC	180
CTCAGAATGT	TGTGGCAGCA	GCTGCTGCCA	AGGCCAAGAT	GGCCACGAGC	ATCCCTGAGC	240
CGGAGGGTGC	AGCTGCTGCC	ACTGCTCAGC	ACAGTGCTGA	GCCCTGGGCC	AGGATGGGAG	300
GCAAGAGGAC	CAAGAAGTCC	AAGCACCTGG	ATGATGAGTA	TGAGAGCAGC	GAGGAGGAGA	360
GAGAGACTCC	CGCGGTCCCCA	CCCACCTGGA	GAGCATCACA	GCCCTCATTTG	ACGGTGC GGG	420
CTCAGTTGGC	CCCTCGGCCC	CCGATGGCCC	CGAGGTCCCCA	GATACCCTCA	AGGCACGTAC	480
TGTGCCTGCC	CCCCCGCAAC	GTGACCCTTC	TGCAGGAGAG	GGCAAATAAG	TTGGTGAAAT	540
ACCTGATGAT	TAAGGACTAC	AAGAAGATCC	CCATCAAGCG	CGCAGACATG	CTGAAGGATG	600
TCATCAGAGA	ATATGATGAA	CATTTCCCTG	AGATCATTGA	ACGAGCAACG	TACACCCTGG	660
AAAAGAAATT	TGGGATCCAC	CTGAAGGAGA	TCGACAAGGA	AGAACACCTG	TATATTCTTG	720
TCTGCACACG	GGACTCCTCA	GCTCGCCTCC	TTGGAAAAAC	CAAGGACACT	CCCAGGCTGA	780
GTCTCTCTTT	GGTGATTCTG	GGCGTCATCT	TCATGAATGG	CAACCGTGCC	AGCGAGGCTG	840
TCCTCTGGGA	GGCACTACGC	AAGATGGGAC	TGCGTCCTGG	GGTGAGACAT	CCCCTCTTTG	900
GAGATCTAAG	GAAACTTCTC	ACCTATGAGT	TTGTAAAGCA	GAAATACCTG	GA CTACAGAC	960
GAGTGCCCAA	CAGCAACCCC	CCGGAGTATG	AGTTCCTCTG	GGGCC'TCCGT	TCCTACCATG	1020
AGACTAGCAA	GATGAAAGTG	CTGAGATTCA	TTGCAGAGGT	TCAGAAAAGA	GACCCTCGTG	1080
ACTGGACTGC	ACAGTTCATG	GAGGCTGCAG	ATGAGGCCTT	GGATGCTCTG	GATGCTGCTG	1140
CAGCTGAGGC	CGAAGCCCGG	GCTGAAGCAA	GAACCCGCAT	GGGAATTGGA	GATGAGGCTG	1200
TGTCTGGGCC	CGGAGCTGGG	ATGACATTGA	GTTTGAGCTG	CTGACCT		1247

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 608993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Pro	Arg	Gly	Gln	Lys	Ser	Lys	Leu	Arg	Ala	Arg	Glu	Lys	Arg	Arg
1				5				10					15		
Lys	Ala	Arg	Glu	Glu	Thr	Gln	Gly	Leu	Lys	Val	Arg	His	Ala	Thr	Ala

				20						25					30
Ala	Glu	Lys	Glu	Glu	Cys	Pro	Ser	Ser	Ser	Pro	Val	Leu	Gly	Asp	Thr
		35					40					45			
Pro	Thr	Ser	Ser	Pro	Ala	Ala	Gly	Ile	Pro	Gln	Lys	Pro	Gln	Gly	Ala
	50				55					60					
Pro	Pro	Thr	Thr	Thr	Ala	Ala	Ala	Ala	Val	Ser	Cys	Thr	Glu	Ser	Asp
65					70					75				80	
Glu	Gly	Ala	Lys	Cys	Gln	Gly	Glu	Glu	Asn	Ala	Ser	Phe	Ser	Gln	Ala
			85						90					95	
Thr	Thr	Ser	Thr	Glu	Ser	Ser	Val	Lys	Asp	Pro	Val	Ala	Trp	Glu	Ala
			100					105					110		
Gly	Met	Leu	Met	His	Phe	Ile	Leu	Arg	Lys	Tyr	Lys	Met	Arg	Glu	Pro
		115					120					125			
Ile	Met	Lys	Ala	Asp	Met	Leu	Lys	Val	Val	Asp	Glu	Lys	Tyr	Lys	Asp
	130					135					140				
His	Phe	Thr	Glu	Ile	Leu	Asn	Gly	Ala	Ser	Arg	Arg	Leu	Glu	Leu	Val
145					150					155					160
Phe	Gly	Leu	Asp	Leu	Lys	Glu	Asp	Asn	Pro	Ser	Ser	His	Thr	Tyr	Thr
			165						170					175	
Leu	Val	Ser	Lys	Leu	Asn	Leu	Thr	Asn	Asp	Gly	Asn	Leu	Ser	Asn	Asp
			180					185					190		
Trp	Asp	Phe	Pro	Arg	Asn	Gly	Leu	Leu	Met	Pro	Leu	Leu	Gly	Val	Ile
		195					200					205			
Phe	Leu	Lys	Gly	Asn	Ser	Ala	Thr	Glu	Glu	Glu	Ile	Trp	Lys	Phe	Met
	210					215					220				
Asn	Val	Leu	Gly	Ala	Tyr	Asp	Gly	Glu	Glu	His	Leu	Ile	Tyr	Gly	Glu
					230					235					240
Pro	Arg	Lys	Phe	Ile	Thr	Gln	Asp	Leu	Val	Gln	Glu	Lys	Tyr	Leu	Lys
				245					250					255	
Tyr	Glu	Gln	Val	Pro	Asn	Ser	Asp	Pro	Pro	Arg	Tyr	Gln	Phe	Leu	Trp
			260					265					270		
Gly	Pro	Arg	Ala	Tyr	Ala	Glu	Thr	Thr	Lys	Met	Lys	Val	Leu	Glu	Phe
		275					280					285			
Leu	Ala	Lys	Met	Asn	Gly	Ala	Thr	Pro	Arg	Asp	Phe	Pro	Ser	His	Tyr
	290					295					300				
Glu	Glu	Ala	Leu	Arg	Asp	Glu	Glu	Glu	Arg	Ala	Gln	Val	Arg	Ser	Ser
305					310					315					320
Val	Arg	Ala	Arg	Arg	Arg	Thr	Thr	Ala	Thr	Thr	Phe	Arg	Ala	Arg	Ser
				325					330					335	
Arg	Ala	Pro	Phe	Ser	Arg	Ser	Ser	His	Pro	Met					
			340					345							

(i) SEQUENCE CHARACTERISTICS:

- (vii) IMMEDIATE SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEO ID NO:4:

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Met	Pro	Arg	Ala	Pro	Lys	Arg	Gln	Arg	Cys	Met	Pro	Glu	Glu	Asp	Leu
1				5					10					15	
Gln	Ser	Gln	Ser	Glu	Thr	Gln	Gly	Leu	Glu	Gly	Ala	Gln	Ala	Pro	Leu
			20					25					30		
Ala	Val	Glu	Glu	Asp	Ala	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Phe
	35						40					45			
Pro	Ser	Ser	Phe	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Cys	Tyr
	50					55					60				
Pro	Leu	Ile	Pro	Ser	Thr	Pro	Glu	Glu	Val	Ser	Ala	Asp	Asp	Glu	Thr
65					70					75				80	
Pro	Asn	Pro	Pro	Gln	Ser	Ala	Gln	Ile	Ala	Cys	Ser	Ser	Pro	Ser	Val
				85					90					95	
Val	Ala	Ser	Leu	Pro	Leu	Asp	Gln	Ser	Asp	Glu	Gly	Ser	Ser	Ser	Gln
			100					105					110		
Lys	Glu	Glu	Ser	Pro	Ser	Thr	Leu	Gln	Val	Leu	Pro	Asp	Ser	Glu	Ser
	115						120					125			
Leu	Pro	Arg	Ser	Glu	Ile	Asp	Glu	Lys	Val	Thr	Asp	Leu	Val	Gln	Phe
	130					135					140				
Leu	Leu	Phe	Lys	Tyr	Gln	Met	Lys	Glu	Pro	Ile	Thr	Lys	Ala	Glu	Ile
145					150					155					160
Leu	Glu	Ser	Val	Ile	Lys	Asn	Tyr	Glu	Asp	His	Phe	Pro	Leu	Leu	Phe
				165					170					175	
Ser	Glu	Ala	Ser	Glu	Cys	Met	Leu	Leu	Val	Phe	Gly	Ile	Asp	Val	Lys
		180					185						190		
Glu	Val	Asp	Pro	Thr	Gly	His	Ser	Phe	Val	Leu	Val	Thr	Ser	Leu	Gly
	195						200					205			
Leu	Thr	Tyr	Asp	Gly	Met	Leu	Ser	Asp	Val	Gln	Ser	Met	Pro	Lys	Thr
	210					215					220				
Gly	Ile	Leu	Ile	Leu	Ile	Leu	Ser	Ile	Ile	Phe	Ile	Glu	Gly	Tyr	Cys
225					230					235					240
Thr	Pro	Glu	Glu	Val	Ile	Trp	Glu	Ala	Leu	Asn	Met	Met	Gly	Leu	Tyr
				245					250					255	
Asp	Gly	Met	Glu	His	Leu	Ile	Tyr	Gly	Glu	Pro	Arg	Lys	Leu	Leu	Thr
		260						265					270		
Gln	Asp	Trp	Val	Gln	Glu	Asn	Tyr	Leu	Glu	Tyr	Arg	Gln	Val	Pro	Gly
	275						280					285			
Ser	Asp	Pro	Ala	Arg	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	His	Ala
	290					295					300				
Glu	Ile	Arg	Lys	Met	Ser	Leu	Leu	Lys	Phe	Leu	Ala	Lys	Val	Asn	Gly
305					310					315					320
Ser	Asp	Pro	Arg	Ser	Phe	Pro	Leu	Trp	Tyr	Glu	Glu	Ala	Leu	Lys	Asp
				325					330					335	
Glu	Glu	Glu	Arg	Ala	Gln	Asp	Arg	Ile	Ala	Thr	Thr	Asp	Asp	Thr	Thr
			340					345					350		
Ala	Met	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Thr	Gly	Ser	Phe	Ser	Tyr	Pro
		355					360					365			
Glu															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1165170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Phe	Ser	Trp	Lys	Ala	Ser	Lys	Ala	Arg	Ser	Pro	Leu	Ser	Pro	Arg
1				5					10					15	
Tyr	Ser	Leu	Pro	Gly	Ser	Thr	Glu	Val	Leu	Thr	Gly	Cys	His	Ser	Tyr
			20					25					30		
Pro	Ser	Arg	Phe	Leu	Ser	Ala	Ser	Ser	Phe	Thr	Ser	Ala	Leu	Ser	Thr
		35					40					45			
Val	Asn	Met	Pro	Arg	Gly	Gln	Lys	Ser	Lys	Thr	Arg	Ser	Arg	Ala	Lys
	50					55					60				
Arg	Gln	Gln	Ser	Arg	Arg	Glu	Val	Pro	Val	Val	Gln	Pro	Thr	Ala	Glu
65					70					75					80
Glu	Ala	Gly	Ser	Ser	Pro	Val	Asp	Gln	Ser	Ala	Gly	Ser	Ser	Phe	Pro
				85					90					95	
Gly	Gly	Ser	Ala	Pro	Gln	Gly	Val	Lys	Thr	Pro	Gly	Ser	Phe	Gly	Ala
			100					105					110		
Gly	Val	Ser	Cys	Thr	Gly	Ser	Gly	Ile	Gly	Gly	Arg	Asn	Ala	Ala	Val
	115						120					125			
Leu	Pro	Asp	Thr	Lys	Ser	Ser	Asp	Gly	Thr	Gln	Ala	Gly	Thr	Ser	Ile
	130					135					140				
Gln	His	Thr	Leu	Lys	Asp	Pro	Ile	Met	Arg	Lys	Ala	Ser	Val	Leu	Ile
145					150					155					160
Glu	Phe	Leu	Leu	Asp	Lys	Phe	Lys	Met	Lys	Glu	Ala	Val	Thr	Arg	Ser
				165					170					175	
Glu	Met	Leu	Ala	Val	Val	Asn	Lys	Lys	Tyr	Lys	Glu	Gln	Phe	Pro	Glu
		180					185						190		
Ile	Leu	Arg	Arg	Thr	Ser	Ala	Arg	Leu	Glu	Leu	Val	Phe	Gly	Leu	Glu
	195						200					205			
Leu	Lys	Glu	Ile	Asp	Pro	Ser	Thr	His	Ser	Tyr	Leu	Leu	Val	Gly	Lys
	210					215					220				
Leu	Gly	Leu	Ser	Thr	Glu	Gly	Ser	Leu	Ser	Ser	Asn	Trp	Gly	Leu	Pro
225					230					235					240
Arg	Thr	Gly	Leu	Leu	Met	Ser	Val	Leu	Gly	Val	Ile	Phe	Met	Lys	Gly
				245					250					255	
Asn	Arg	Ala	Thr	Glu	Gln	Glu	Val	Trp	Gln	Phe	Leu	His	Gly	Val	Gly
			260					265					270		
Val	Tyr	Ala	Gly	Lys	Lys	His	Leu	Ile	Phe	Gly	Glu	Pro	Glu	Glu	Phe
	275						280					285			
Ile	Arg	Asp	Val	Val	Arg	Glu	Asn	Tyr	Leu	Glu	Tyr	Arg	Gln	Val	Pro
	290					295					300				
Gly	Ser	Asp	Pro	Pro	Ser	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	His
305					310					315					320
Ala	Glu	Thr	Thr	Lys	Met	Lys	Val	Leu	Glu	Val	Leu	Ala	Lys	Val	Asn
				325					330					335	
Gly	Thr	Val	Pro	Ser	Ala	Phe	Pro	Asn	Leu	Tyr	Gln	Leu	Ala	Leu	Arg
			340					345					350		
Asp	Gln	Ala	Gly	Gly	Val	Pro	Arg	Arg	Arg	Val	Gln	Gly	Lys	Gly	Val
	355						360					365			
His	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Ser	Ser	Asn	Met				

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380

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1040691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gln	Ser	Lys	Asp	Leu	Ser	Asp	Pro	Asn	Phe	Ala	Ala	Glu
1				5					10					15	
Ala	Pro	Asp	Cys	Glu	Met	Gln	Asp	Ser	Asp	Ala	Val	Pro	Val	Gly	Ile
		20						25					30		
Pro	Pro	Pro	Ala	Ser	Leu	Ala	Ala	Asn	Leu	Ala	Gly	Pro	Pro	Cys	Ala
		35					40					45			
Pro	Glu	Gly	Pro	Met	Ala	Ala	Gln	Gln	Ala	Ser	Pro	Pro	Pro	Glu	Glu
	50					55					60				
Arg	Ile	Glu	Asp	Val	Asp	Pro	Lys	Ile	Leu	Gln	Gln	Ala	Ala	Glu	Glu
65					70					75				80	
Gly	Arg	Ala	His	Gln	Pro	Gln	Ser	Pro	Ala	Arg	Pro	Ile	Pro	Ala	Pro
			85						90					95	
Pro	Ala	Pro	Ala	Gln	Leu	Val	Gln	Lys	Ala	His	Glu	Leu	Met	Trp	Tyr
			100					105					110		
Val	Leu	Val	Lys	Asp	Gln	Lys	Arg	Met	Val	Leu	Trp	Phe	Pro	Asp	Met
		115					120					125			
Val	Lys	Glu	Val	Met	Gly	Ser	Tyr	Lys	Lys	Trp	Cys	Arg	Ser	Ile	Leu
	130					135					140				
Arg	Arg	Thr	Ser	Val	Ile	Leu	Ala	Arg	Val	Phe	Gly	Leu	His	Leu	Arg
145					150					155				160	
Leu	Thr	Asn	Leu	His	Thr	Met	Glu	Phe	Ala	Leu	Val	Lys	Ala	Leu	Ser
			165						170					175	
Pro	Glu	Glu	Leu	Asp	Arg	Val	Ala	Leu	Asn	Asn	Arg	Met	Pro	Met	Thr
		180						185					190		
Gly	Leu	Leu	Leu	Met	Ile	Leu	Ser	Leu	Ile	Tyr	Val	Lys	Gly	Arg	Gly
	195						200					205			
Ala	Arg	Glu	Gly	Ala	Val	Trp	Asn	Val	Leu	Arg	Ile	Leu	Gly	Leu	Arg
	210					215					220				
Pro	Trp	Lys	Lys	His	Ser	Thr	Phe	Gly	Asp	Val	Arg	Lys	Ile	Ile	Thr
225					230					235				240	
Glu	Glu	Phe	Val	Gln	Gln	Asn	Tyr	Leu	Lys	Tyr	Gln	Arg	Val	Pro	His
			245						250					255	
Ile	Glu	Pro	Pro	Glu	Tyr	Glu	Phe	Phe	Trp	Gly	Ser	Arg	Ala	Asn	Arg
		260						265					270		
Glu	Ile	Thr	Lys	Met	Gln	Ile	Met	Glu	Phe	Leu	Ala	Arg	Val	Phe	Lys
	275						280					285			
Lys	Asp	Pro	Gln	Ala	Trp	Pro	Ser	Arg	Tyr	Arg	Glu	Ala	Leu	Glu	Gln
	290					295					300				
Ala	Arg	Ala	Leu	Arg	Glu	Ala	Asn	Leu	Ala	Ala	Gln	Ala	Pro	Arg	Ser

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310

315

320

Ser Val Ser Glu Asp  
325